

# Resource Summary Report

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## GOSlimViewer

RRID:SCR\_005665

Type: Tool

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### Proper Citation

GOSlimViewer (RRID:SCR\_005665)

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### Resource Information

**URL:** [http://agbase.msstate.edu/cgi-bin/tools/goslimviewer\\_select.pl](http://agbase.msstate.edu/cgi-bin/tools/goslimviewer_select.pl)

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**Description:** Service to summarize the GO function associated with a data set using prepared GO Slim sets. The input is a tab separated list of gene product IDs and GO IDs.

**Abbreviations:** GOSlimViewer

**Synonyms:** GO Slim Viewer, GOSlim Viewer

**Resource Type:** analysis service resource, data analysis service, production service resource, service resource

**Defining Citation:** [PMID:17135208](#), [PMID:16961921](#)

**Keywords:** agriculture, browser, slimmer-type tool, gene ontology, gene, ontology, ontology or annotation browser

**Funding:** USDA ;  
Mississippi State University; Mississippi; USA ;  
MSU Office of Research ;  
MSU Bagley College of Engineering ;  
MSU College of College of Veterinary Medicine ;  
MSU Life Science and Biotechnology Institute

**Availability:** Free for academic use

**Resource Name:** GOSlimViewer

**Resource ID:** SCR\_005665

**Alternate IDs:** nlx\_149103, OMICS\_02270

**Record Creation Time:** 20220129T080231+0000

**Record Last Update:** 20260808T190404+0000

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## Ratings and Alerts

No rating or validation information has been found for GOSlimViewer.

No alerts have been found for GOSlimViewer.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 40 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

Coates BS, et al. (2023) A draft *Diabrotica virgifera virgifera* genome: insights into control and host plant adaption by a major maize pest insect. *BMC genomics*, 24(1), 19.

Escobar-Niño A, et al. (2023) The Adaptation of *Botrytis cinerea* Extracellular Vesicles Proteome to Surrounding Conditions: Revealing New Tools for Its Infection Process. *Journal of fungi* (Basel, Switzerland), 9(9).

Urban MO, et al. (2021) The Resistance of Oilseed Rape Microspore-Derived Embryos to Osmotic Stress Is Associated With the Accumulation of Energy Metabolism Proteins, Redox Homeostasis, Higher Absciscic Acid, and Cytokinin Contents. *Frontiers in plant science*, 12, 628167.

Xie Y, et al. (2020) Transcriptome differences in adipose stromal cells derived from pre- and postmenopausal women. *Stem cell research & therapy*, 11(1), 92.

Liu X, et al. (2020) Genetic mapping and genomic selection for maize stalk strength. *BMC plant biology*, 20(1), 196.

Human MP, et al. (2020) Time-Course RNAseq Reveals *Exserohilum turcicum* Effectors and Pathogenicity Determinants. *Frontiers in microbiology*, 11, 360.

Hewel C, et al. (2019) Common miRNA Patterns of Alzheimer's Disease and Parkinson's Disease and Their Putative Impact on Commensal Gut Microbiota. *Frontiers in neuroscience*, 13, 113.

Marks RA, et al. (2019) Genome of the tropical plant *Marchantia inflexa*: implications for sex chromosome evolution and dehydration tolerance. *Scientific reports*, 9(1), 8722.

Rashmi D, et al. (2019) Integrative omics analysis in *Pandanus odorifer* (Forssk.) Kuntze reveals the role of Asparagine synthetase in salinity tolerance. *Scientific reports*, 9(1), 932.

Ma Y, et al. (2019) A pan-transcriptome analysis shows that disease resistance genes have undergone more selection pressure during barley domestication. *BMC genomics*, 20(1), 12.

Zhang C, et al. (2018) Transcriptional and physiological data reveal the dehydration memory behavior in switchgrass (*Panicum virgatum* L.). *Biotechnology for biofuels*, 11, 91.

Zhang C, et al. (2018) Long non-coding RNAs of switchgrass (*Panicum virgatum* L.) in multiple dehydration stresses. *BMC plant biology*, 18(1), 79.

Qin L, et al. (2017) Proteomic analysis of macrophage in response to *Edwardsiella tarda* infection. *Microbial pathogenesis*, 111, 86.

Straub D, et al. (2017) Cross-Species Genome-Wide Identification of Evolutionary Conserved MicroProteins. *Genome biology and evolution*, 9(3), 777.

Urban MO, et al. (2017) Proteomic and physiological approach reveals drought-induced changes in rapeseeds: Water-saver and water-spender strategy. *Journal of proteomics*, 152, 188.

Xue M, et al. (2017) Analysis of the spleen proteome of chickens infected with reticuloendotheliosis virus. *Archives of virology*, 162(5), 1187.

Cheon SA, et al. (2017) A novel bZIP protein, Gsb1, is required for oxidative stress response, mating, and virulence in the human pathogen *Cryptococcus neoformans*. *Scientific reports*, 7(1), 4044.

Schwager EE, et al. (2017) The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. *BMC biology*, 15(1), 62.

Nayak SN, et al. (2017) *Aspergillus flavus* infection triggered immune responses and host-pathogen cross-talks in groundnut during in-vitro seed colonization. *Scientific reports*, 7(1), 9659.

Malhotra S, et al. (2017) Decoding the similarities and differences among mycobacterial species. *PLoS neglected tropical diseases*, 11(8), e0005883.